SEQUENCE LISTING

(1) GENERAL INFORMATION:

　(i i i) NUMBER OF SEQUENCES: 14

(2) INFORMATION FOR SEQ ID NO:1:

　　(i) SEQUENCE CHARACTERISTICS:
　　　　(A) LENGTH: 24 bases
　　　　(B) TYPE: nucleic acid
　　　　(C) STRANDEDNESS: single
　　　　(D) TOPOLOGY: linear

　　(i i) MOLECULE TYPE: DNA (genomic)

　　(x i) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGCCCAGCTC CTGGCCCGCC GCTT

24

(2) INFORMATION FOR SEQ ID NO:2:

　　(i) SEQUENCE CHARACTERISTICS:
　　　　(A) LENGTH: 24 bases
　　　　(B) TYPE: nucleic acid
　　　　(C) STRANDEDNESS: single
　　　　(D) TOPOLOGY: linear

　　(i i) MOLECULE TYPE: DNA (genomic)

　　(x i) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGCATCAAC ACAGGCGCCT CTTC

24

(2) INFORMATION FOR SEQ ID NO:3:

　　(i) SEQUENCE CHARACTERISTICS:
　　　　(A) LENGTH: 27 bases
　　　　(B) TYPE: nucleic acid
　　　　(C) STRANDEDNESS: single
　　　　(D) TOPOLOGY: linear

　　(i i) MOLECULE TYPE: DNA (genomic)

　　(x i) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTCAAATGAG ATTGTGGGAA AATTGCT

27

(2) INFORMATION FOR SEQ ID NO:4:

　　(i) SEQUENCE CHARACTERISTICS:
　　　　(A) LENGTH: 24 bases
　　　　(B) TYPE: nucleic acid
　　　　(C) STRANDEDNESS: single
　　　　(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGATCATCTC TGCCTGAGTA TCTT   24

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (i i) MOLECULE TYPE: DNA (genomic)

    (x i) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCACCCATGG CAAATTCCAT GGCA   24

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (i i) MOLECULE TYPE: DNA (genomic)

    (x i) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCTAGACGGC AGGTCAGGTC CACC   24

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (i i) MOLECULE TYPE: protein

    (x i) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp Asp Ile Asn Pro Thr Val Leu Leu Lys Glu Arg
1   5   10

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (i i) MOLECULE TYPE: DNA (genomic)

    (x i) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTGCGATGCT CGCCCGCGCC CTG   23

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (i i) MOLECULE TYPE: DNA (genomic)

    (x i) SEQUENCE DESCRIPTION: SEQ ID NO:9:

-continued

CTTCTACAGT TCAGTCGAAC GTTC   24

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 604 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (i i) MOLECULE TYPE: protein

    (x i) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
Met Leu Ala Arg Ala Leu Leu Leu Cys Ala Val Leu Ala Leu Ser His
1                   5                   10                  15

Thr Ala Asn Pro Cys Cys Ser His Pro Cys Gln Asn Arg Gly Val Cys
                20                  25                  30

Met Ser Val Gly Phe Asp Gln Tyr Lys Cys Asp Cys Thr Arg Thr Gly
            35                  40                  45

Phe Tyr Gly Glu Asn Cys Ser Thr Pro Glu Phe Leu Thr Arg Ile Lys
    50                  55                  60

Leu Phe Leu Lys Pro Thr Pro Asn Thr Val His Tyr Ile Leu Thr His
65                  70                  75                  80

Phe Lys Gly Phe Trp Asn Val Val Asn Asn Ile Pro Phe Leu Arg Asn
                85                  90                  95

Ala Ile Met Ser Tyr Val Leu Thr Ser Arg Ser His Leu Ile Asp Ser
                100                 105                 110

Pro Pro Thr Tyr Asn Ala Asp Tyr Gly Tyr Lys Ser Trp Glu Ala Phe
            115                 120                 125

Ser Asn Leu Ser Tyr Tyr Thr Arg Ala Leu Pro Pro Val Pro Asp Asp
    130                 135                 140

Cys Pro Thr Pro Leu Gly Val Lys Gly Lys Lys Gln Leu Pro Asp Ser
145                 150                 155                 160

Asn Glu Ile Val Glu Lys Leu Leu Leu Arg Arg Lys Phe Ile Pro Asp
                165                 170                 175

Pro Gln Gly Ser Asn Met Met Phe Ala Phe Phe Ala Gln His Phe Thr
            180                 185                 190

His Gln Phe Phe Lys Thr Asp His Lys Arg Gly Pro Ala Phe Thr Asn
            195                 200                 205

Gly Leu Gly His Gly Val Asp Leu Asn His Ile Tyr Gly Gln Thr Leu
    210                 215                 220

Ala Arg Gln Arg Lys Leu Arg Leu Phe Lys Asp Gly Lys Met Lys Tyr
225                 230                 235                 240

Gln Ile Ile Asp Gly Glu Met Tyr Pro Pro Thr Val Lys Asp Thr Gln
                245                 250                 255

Ala Gln Met Ile Tyr Pro Pro Gln Val Pro Glu His Leu Arg Phe Ala
            260                 265                 270

Val Gly Gln Glu Val Phe Gly Leu Val Pro Gly Leu Met Met Tyr Ala
            275                 280                 285

Thr Ile Trp Leu Arg Glu His Asn Arg Val Cys Asp Val Leu Lys Gln
    290                 295                 300

Glu His Pro Glu Trp Gly Asp Glu Gln Leu Phe Gln Thr Ser Arg Leu
305                 310                 315                 320

Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile Glu Asp Tyr Val Gln
                325                 330                 335

His Leu Ser Gly Tyr His Phe Lys Leu Lys Phe Asp Pro Gln Leu Leu
```

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```
                340                    345                    350

    Phe Asn Lys Gln Phe Gln Tyr Gln Asn Arg Ile Ala Ala Glu Phe Asn
            355                    360                    365

    Thr Leu Tyr His Trp His Pro Leu Leu Pro Asp Thr Phe Gln Ile His
        370                    375                    380

    Asp Gln Lys Tyr Asn Tyr Gln Gln Phe Ile Tyr Asn Asn Ser Ile Leu
    385                    390                    395                    400

    Leu Glu His Gly Ile Thr Gln Phe Val Glu Ser Phe Thr Arg Gln Ile
                    405                    410                    415

    Ala Gly Arg Val Ala Gly Gly Arg Asn Val Pro Pro Ala Val Gln Lys
                420                    425                    430

    Val Ser Gln Ala Ser Ile Asp Gln Ser Arg Gln Met Lys Tyr Gln Ser
            435                    440                    445

    Phe Asn Glu Tyr Arg Lys Arg Phe Met Leu Lys Pro Tyr Gln Ser Phe
        450                    455                    460

    Gln Glu Leu Thr Gly Glu Lys Glu Met Ser Ala Glu Leu Glu Ala Leu
    465                    470                    475                    480

    Tyr Gly Asp Ile Asp Ala Val Glu Leu Tyr Pro Ala Leu Leu Val Glu
                    485                    490                    495

    Lys Pro Arg Pro Asp Ala Ile Phe Gly Glu Thr Met Val Glu Val Gly
                500                    505                    510

    Ala Pro Phe Ser Leu Lys Gly Leu Met Gly Asn Val Ile Cys Ser Pro
            515                    520                    525

    Ala Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu Val Gly Phe Gln Ile
        530                    535                    540

    Ile Asn Thr Ala Ser Ile Gln Ser Leu Ile Cys Asn Asn Val Lys Gly
    545                    550                    555                    560

    Cys Pro Phe Thr Ser Phe Ser Val Pro Asp Pro Glu Leu Ile Lys Thr
                    565                    570                    575

    Val Thr Ile Asn Ala Ser Ser Ser Arg Ser Gly Leu Asp Asp Ile Asn
                580                    585                    590

    Pro Thr Val Leu Leu Lys Gln Arg Ser Thr Glu Leu
                595                    600
```

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3387 bases
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (i i) MOLECULE TYPE: DNA (genomic)

    (x i) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
GTCCAGGAAC TCCTCAGCAG CGCCTCCTTC AGCTCCACAG CCAGACGCCC TCAGACAGCA      60

AAGCCTACCC CCGCGCCGCG CCCTGCCCGC CGCTGCGATG CTCGCCCGCG CCCTGCTGCT     120

GTGCGCGGTC CTGGCGCTCA GCCATACAGC AAATCCTTGC TGTTCCCACC CATGTCAAAA     180

CCGAGGTGTA TGTATGAGTG TGGGATTTGA CCAGTATAAG TGCGATTGTA CCCGGACAGG     240

ATTCTATGGA GAAAACTGCT CAACACCGGA ATTTTTGACA AGAATAAAAT TATTTCTGAA     300

ACCCACTCCA AACACAGTGC ACTACATACT TACCCACTTC AAGGGATTTT GGAACGTTGT     360

GAATAACATT CCCTTCCTTC GAAATGCAAT TATGAGTTAT GTGTTGACAT CCAGATCACA     420

TTTGATTGAC AGTCCACCAA CTTACAATGC TGACTATGGC TACAAAAGCT GGGAAGCCTT     480

CTCTAACCTC TCCTATTATA CTAGAGCCCT TCCTCCTGTG CCTGATGATT GCCCGACTCC     540
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CTTGGGTGTC AAAGGTAAAA AGCAGCTTCC TGATTCAAAT GAGATTGTGG AAAAATTGCT     600
TCTAAGAAGA AAGTTCATCC CTGATCCCCA GGGCTCAAAC ATGATGTTTG CATTCTTTGC     660
CCAGCACTTC ACGCACCAGT TTTTCAAGAC AGATCATAAG CGAGGGCCAG CTTTCACCAA     720
CGGGCTGGGC CATGGGGTGG ACTTAAATCA TATTTACGGT GAAACTCTGG CTAGACAGCG     780
TAAACTGCGC CTTTTCAAGG ATGGAAAAAT GAAATATCAG ATAATTGATG GAGAGATGTA     840
TCCTCCCACA GTCAAAGATA CTCAGGCAGA GATGATCTAC CCTCCTCAAG TCCCTGAGCA     900
TCTACGGTTT GCTGTGGGGC AGGAGGTCTT TGGTCTGGTG CCTGGTCTGA TGATGTATGC     960
CACAATCTGG CTGCGGGAAC ACAACAGAGT ATGTGATGTG CTTAAACAGG AGCATCCTGA    1020
ATGGGGTGAT GAGCAGTTGT TCCAGACAAG CAGGCTAATA CTGATAGGAG AGACTATTAA    1080
GATTGTGATT GAAGATTATG TGCAACACTT GAGTGGCTAT CACTTCAAAC TGAAATTTGA    1140
CCCAGAACTA CTTTTCAACA AACAATTCCA GTACCAAAAT CGTATTGCTG CTGAATTTAA    1200
CACCCTCTAT CACTGGCATC CCCTTCTGCC TGACACCTTT CAAATTCATG ACCAGAAATA    1260
CAACTATCAA CAGTTTATCT ACAACAACTC TATATTGCTG GAACATGGAA TTACCCAGTT    1320
TGTTGAATCA TTCACCAGGC AAATTGCTGG CAGGGTTGCT GGTGGTAGGA ATGTTCCACC    1380
CGCAGTACAG AAAGTATCAC AGGCTTCCAT TGACCAGAGC AGGCAGATGA AATACCAGTC    1440
TTTTAATGAG TACCGCAAAC GCTTTATGCT GAAGCCCTAT GAATCATTTG AAGAACTTAC    1500
AGGAGAAAAG GAAATGTCTG CAGAGTTGGA AGCACTCTAT GGTGACATCG ATGCTGTGGA    1560
GCTGTATCCT GCCCTTCTGG TAGAAAAGCC TCGGCCAGAT GCCATCTTTG GTGAAACCAT    1620
GGTAGAAGTT GGAGCACCAT TCTCCTTGAA AGGACTTATG GGTAATGTTA TATGTTCTCC    1680
TGCCTACTGG AAGCCAAGCA CTTTTGGTGG AGAAGTGGGT TTTCAAATCA TCAACACTGC    1740
CTCAATTCAG TCTCTCATCT GCAATAACGT GAAGGGCTGT CCCTTTACTT CATTCAGTGT    1800
TCCAGATCCA GAGCTCATTA AAACAGTCAC CATCAATGCA AGTTCTTCCC GCTCCGGACT    1860
AGATGATATC AATCCCACAG TACTACTAAA AGAACGGTCG ACTGAACTGT AGAAGTCTAA    1920
TGATCATATT TATTTATTTA TATGAACCAT GTCTATTAAT TTAATTATTT AATAATATTT    1980
ATATTAAACT CCTTATGTTA CTTAACATCT TCTGTAACAG AAGTCAGTAC TCCTGTTGCG    2040
GAGAAAGGAG TCATACTTGT GAAGACTTTT ATGTCACTAC TCTAAAGATT TTGCTGTTGC    2100
TGTTAAGTTT GGAAAACAGT TTTTATTCTG TTTTATAAAC CAGAGAGAAA TGAGTTTTGA    2160
CGTCTTTTTA CTTGAATTTC AACTTATATT ATAAGGACGA AAGTAAAGAT GTTTGAATAC    2220
TTAAACACTA TCACAAGATG CCAAAATGCT GAAAGTTTTT ACACTGTCGA TGTTTCCAAT    2280
GCATCTTCCA TGATGCATTA GAAGTAACTA ATGTTTGAAA TTTTAAAGTA CTTTTGGGTA    2340
TTTTTCTGTC ATCAAACAAA ACAGGTATCA GTGCATTATT AAATGAATAT TTAAATTAGA    2400
CATTACCAGT AATTTCATGT CTACTTTTTA AAATCAGCAA TGAAACAATA ATTTGAAATT    2460
TCTAAATTCA TAGGGTAGAA TCACCTGTAA AAGCTTGTTT GATTTCTTAA AGTTATTAAA    2520
CTTGTACATA TACCAAAAAG AAGCTGTCTT GGATTTAAAT CTGTAAAATC AGATGAAATT    2580
TTACTACAAT TGCTTGTTAA AATATTTTAT AAGTGATGTT CCTTTTTCAC CAAGAGTATA    2640
AACCTTTTTA GTGTGACTGT TAAAACTTCC TTTTAAATCA AAATGCCAAA TTTATTAAGG    2700
TGGTGGAGCC ACTGCAGTGT TATCTCAAAA TAAGAATATC CTGTTGAGAT ATTCCAGAAT    2760
CTGTTTATAT GGCTGGTAAC ATGTAAAAAC CCCATAACCC CGCCAAAAGG GGTCCTACCC    2820
TTGAACATAA AGCAATAACC AAAGGAGAAA AGCCCAAATT ATTGGTTCCA AATTTAGGGT    2880
TTAAACTTTT TGAAGCAAAC TTTTTTTTAG CCTTGTGCAC TGCAGACCTG GTACTCAGAT    2940
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TTTGCTATGA GGTTAATGAA GTACCAAGCT GTGCTTGAAT AACGATATGT TTTCTCAGAT    3000

TTTCTGTTGT ACAGTTTAAT TTAGCAGTCC ATATCACATT GCAAAAGTAG CAATGACCTC    3060

ATAAAATACC TCTTCAAAAT GCTTAAATTC ATTTCACACA TTAATTTTAT CTCAGTCTTG    3120

AAGCCAATTC AGTAGGTGCA TTGGAATCAA GCCTGGCTAC CTGCATGCTG TTCCTTTTCT    3180

TTTCTTCTTT TAGCCATTTT GCTAAGAGAC ACAGTCTTCT CAAACACTTC GTTTCTCCTA    3240

TTTTGTTTTA CTAGTTTTAA GATCAGAGTT CACTTTCTTT GGACTCTGCC TATATTTTCT    3300

TACCTGAACT TTTGCAAGTT TTCAGGTAAA CCTCAGCTCA GGACTGCTAT TTAGCTCCTC    3360

TTAAGAAGAT TAAAAAAAAA AAAAAAG                                       3387
```

(2) INFORMATION FOR SEQ ID NO:12:

 (i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 21 bases
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

 (i i) MOLECULE TYPE: DNA (genomic)

 (x i) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
CCTTCCTTCG AAATGCAATT A                                              21
```

(2) INFORMATION FOR SEQ ID NO:13:

 (i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 21 bases
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

 (i i) MOLECULE TYPE: DNA (genomic)

 (x i) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
AAACTGATGC GTGAAGTGCT G                                              21
```

(2) INFORMATION FOR SEQ ID NO:14:

 (i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 21 bases
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: single
  (D) TOPOLOGY: linear

 (i i) MOLECULE TYPE: DNA (genomic)

 (x i) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
GAGATTGTGG GAAAATTGCT T                                              21
```